IN THE SPECIFICATION

Please amend the specification as follows:

In the paragraph on page 4, beginning on line 1...

--containing 0.1% TFA. The flow rate was maintained at 1ml min^{-1} and the absorbance was monitored at 226 nm. Fractionation into several peptide components was achieved. The peptide components were analyzed by MALDI mass spectra analysis of individual HPLC fractions. The intense component at the retention time of 23.4 minutes corresponding to a molecular mass of 1659 Da was chosen for mass spectrometric denovo sequencing. The peptide component showed a high resolution MALDI mass spectrum, which establishes [M+H]+ = 1659.1 Da (monoisotopic mass). The inset shows the charge states observed in an electrospray mass spectrum, where the +2 and +3 states are detectable suggesting the presence of at least three protonatable groups in the molecule. Attempted reduction with DTT followed by alkylation with iodoacetamide left the molecular mass unchanged, establishing the *absence* of disulfide bonds. Acetylation with acetic anhydride and acetic acid yielded a product with a mass [M+H]+ = 1701.3 Da (Δm = +42Da) indicating the presence of a single primary amino group. UV and fluorescence spectra established the presence of both Trp and Tyr residues. Peptide sequencing was undertaken using MALDI MS/MS techniques selecting the 1659.1 Da as the precursor ion. Figure 3 shows the observed fragment ions along with assignments of the b and y ion series (13). The presence of an intense b2 ion at 285 Da permitted sequential tracing of the 8-residue segment –GGSWYRFP- (residues 3 to 10 of SEQ ID NO: 1). The immonium ions at 70, 110, 136 and 159 suggested the presence of the residues Pro, His, Tyr and Trp, respectively. The b2 ion at 285 Da could correspond to the dipeptide –FH- or –HF- at the amino terminus. The observation of mass peaks at 194.9 Da suggested the presence of the dipeptide ion –GH- or –HG-. This supports the assignment of the sequence –FHG- at the N-terminus. The paucity of intense fragments in the mass range 1200 – 1500 Da limited extension of the sequence at the C-terminus.--

In the paragraph beginning at line 1 on page 6:

--corresponds to a facile loss of NH3 from the C-terminus suggestive of the presence of C-terminal amidation. *Conus* peptides are often posttranslationally modified, with amidation being

commonly observed (14,15). The identification of the b2 ion at 245 Da corresponds to the –FP- fragment, already established by MALDI MS/MS, permitting the ready identification of the C-terminus tripeptide as -WGY-amide. The final determined sequence is FHGGSWYRFPWGY-NH2 (SEQ ID NO: 1), corresponding to a calculated average mass of 1659.8 Da (Average mass observed in ESI MS = 1659.3 Da).

In the paragraph beginning on line 18 of page 7:

Prosite was also used to search for the following variant:

[FY]-H-G-G-S-W-[YF]-[RK]-[FY]-P-W-G-[YF] (SEQ ID NO: 1)

No hits were found.